

DKRUSE

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OIPE

9-27-01

RAW SEQUENCE LISTING

DATE: 07/25/2001

PATENT APPLICATION: US/09/453,387A

TIME: 15:26:46

Input Set : A:\Uco-956.app

Output Set: N:\CRF3\07252001\I453387A.raw

PS

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3 <110> APPLICANT: Wilkins, Thea A.
 4 The Regents of the University of California
 6 <120> TITLE OF INVENTION: Cotton Transcription Factors and Their Uses
 8 <130> FILE REFERENCE: 023070-095600US
 10 <140> CURRENT APPLICATION NUMBER: US 09/453,387A
 11 <141> CURRENT FILING DATE: 1999-12-02
 13 <160> NUMBER OF SEQ ID NOS: 26
 15 <170> SOFTWARE: PatentIn Ver. 2.1
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 1006
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Gossypium hirsutum
 22 <220> FEATURE:
 23 <221> NAME/KEY: CDS
 24 <222> LOCATION: (59)..(943)
 25 <223> OTHER INFORMATION: GhMYB1
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 31 Met Gly Arg Ser Pro Cys Cys Glu Lys Ala His Thr Asn Lys Gly Ala
 32 1 5 10 15
 34 tgg acc aaa gag gaa gat caa cgc ctc atc aac tac atc cgt gtc cat 154
 35 Trp Thr Lys Glu Glu Asp Gln Arg Leu Ile Asn Tyr Ile Arg Val His
 36 20 25 30
 38 ggt gaa ggc tgc tgg cgt tcc ctc ccc aaa gct gct ggg ctg ctt aga 202
 39 Gly Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu Leu Arg
 40 35 40 45
 42 tgt ggt aag agt tgc aga tta aga tgg ata aac tac ttg agg cct gat 250
 43 Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
 44 50 55 60
 46 ctt aag aga gga aat ttc act gaa gaa gaa gat gag ctt atc atc aag 298
 47 Leu Lys Arg Gly Asn Phe Thr Glu Glu Glu Asp Glu Leu Ile Ile Lys
 48 65 70 75 80
 50 ctt cac agt tta ctt gga aac aaa tgg tca ttg att gct gga aga tta 346
 51 Leu His Ser Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Gly Arg Leu
 52 85 90 95
 54 cca gga aga aca gat aat gag ata aag aac tac tgg aac aca cac atc 394
 55 Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile
 56 100 105 110
 58 aaa aga aag ctt ata agc aga gga att gat cca caa act cat cgt cct 442
 59 Lys Arg Lys Leu Ile Ser Arg Gly Ile Asp Pro Gln Thr His Arg Pro
 60 115 120 125
 62 ctc aat caa acg gcc aat acc aac aca gtc aca gcc ccc acc gaa ttg 490
 63 Leu Asn Gln Thr Ala Asn Thr Asn Thr Val Thr Ala Pro Thr Glu Leu
 64 130 135 140
 66 gat ttc aga aac tcg ccc aca tcc gtt tcc aaa tcc agt tcc atc aaa 538
 67 Asp Phe Arg Asn Ser Pro Thr Ser Val Ser Lys Ser Ser Ser Ile Lys

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68 145          150          155          160
70 aac ccg tct ctg gat ttc aat tac aat gaa ttt caa ttc aag tcc aac 586
71 Asn Pro Ser Leu Asp Phe Asn Tyr Asn Glu Phe Gln Phe Lys Ser Asn
72          165          170          175
74 aca gat tcc ctt gaa gaa ccc aac tgt aca gcc agc agt ggc atg act 634
75 Thr Asp Ser Leu Glu Glu Pro Asn Cys Thr Ala Ser Ser Gly Met Thr
76          180          185          190
78 aca gat gaa gag caa caa gaa cag ctg cac aag aag cag caa tac ggt 682
79 Thr Asp Glu Glu Gln Gln Glu Gln Leu His Lys Lys Gln Gln Tyr Gly
80          195          200          205
82 ccg agc aat ggg caa gac ata aat ttg gag ctg tcg att ggg att gtt 730
83 Pro Ser Asn Gly Gln Asp Ile Asn Leu Glu Leu Ser Ile Gly Ile Val
84          210          215          220
86 tca gct gac tca tct cgg gta tca aat gcc aac tcg gcc gag tcg aaa 778
87 Ser Ala Asp Ser Ser Arg Val Ser Asn Ala Asn Ser Ala Glu Ser Lys
88 225          230          235          240
90 cca aag gta gat aac aac aat ttc cag ttt ctt gaa caa gct atg gtg 826
91 Pro Lys Val Asp Asn Asn Asn Phe Gln Phe Leu Glu Gln Ala Met Val
92          245          250          255
94 gct aag gcg gta tgt ttg tgt tgg caa tta ggt ttt gga aca agt gaa 874
95 Ala Lys Ala Val Cys Leu Cys Trp Gln Leu Gly Phe Gly Thr Ser Glu
96          260          265          270
98 att tgt agg aac tgt caa aat tca aat tca aat ggc ttc tat agt tat 922
99 Ile Cys Arg Asn Cys Gln Asn Ser Asn Ser Asn Gly Phe Tyr Ser Tyr
100          275          280          285
102 tgt aga ccc ttg gat tca tag ggtcatcttt ttcttctttc ttctgtttt 973
103 Cys Arg Pro Leu Asp Ser
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110 <211> LENGTH: 294
111 <212> TYPE: PRT
112 <213> ORGANISM: Gossypium hirsutum
114 <400> SEQUENCE: 2
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117 Trp Thr Lys Glu Glu Asp Gln Arg Leu Ile Asn Tyr Ile Arg Val His
118          20          25          30
119 Gly Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu Leu Arg
120          35          40          45
121 Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
122          50          55          60
123 Leu Lys Arg Gly Asn Phe Thr Glu Glu Glu Asp Glu Leu Ile Ile Lys
124 65          70          75          80
125 Leu His Ser Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Gly Arg Leu
126          85          90          95
127 Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile
128          100          105          110
129 Lys Arg Lys Leu Ile Ser Arg Gly Ile Asp Pro Gln Thr His Arg Pro

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130          115          120          125
131 Leu Asn Gln Thr Ala Asn Thr Asn Thr Val Thr Ala Pro Thr Glu Leu
132          130          135          140
133 Asp Phe Arg Asn Ser Pro Thr Ser Val Ser Lys Ser Ser Ser Ile Lys
134 145          150          155          160
135 Asn Pro Ser Leu Asp Phe Asn Tyr Asn Glu Phe Gln Phe Lys Ser Asn
136          165          170          175
137 Thr Asp Ser Leu Glu Glu Pro Asn Cys Thr Ala Ser Ser Gly Met Thr
138          180          185          190
139 Thr Asp Glu Glu Gln Gln Glu Gln Leu His Lys Lys Gln Gln Tyr Gly
140          195          200          205
141 Pro Ser Asn Gly Gln Asp Ile Asn Leu Glu Leu Ser Ile Gly Ile Val
142          210          215          220
143 Ser Ala Asp Ser Ser Arg Val Ser Asn Ala Asn Ser Ala Glu Ser Lys
144 225          230          235          240
145 Pro Lys Val Asp Asn Asn Asn Phe Gln Phe Leu Glu Gln Ala Met Val
146          245          250          255
147 Ala Lys Ala Val Cys Leu Cys Trp Gln Leu Gly Phe Gly Thr Ser Glu
148          260          265          270
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150          275          280          285
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152          290
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161 <220> FEATURE:
162 <221> NAME/KEY: CDS
163 <222> LOCATION: (72)..(752)
164 <223> OTHER INFORMATION: GhMYB6
166 <400> SEQUENCE: 3
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170          Met Arg Lys Pro Cys Cys Asp Lys Gln Gly Thr Asn Lys
171          1          5          10
173 gga gcc tgg tcc aag caa gaa gat caa aag ctc att gat tat ata cgt 158
174 Gly Ala Trp Ser Lys Gln Glu Asp Gln Lys Leu Ile Asp Tyr Ile Arg
175          15          20          25
177 att cat ggt gaa ggc tgt tgg cgt tcc ctc ccc aaa gct gca ggt ttg 206
178 Ile His Gly Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu
179 30          35          40          45
181 cac cgt tgc ggt aaa agt tgc agg ctg aga tgg ata aat tac tta aga 254
182 His Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg
183          50          55          60
185 cca gat atc aaa cgt ggt aac ttt gct caa gac gaa gag gac tta att 302
186 Pro Asp Ile Lys Arg Gly Asn Phe Ala Gln Asp Glu Glu Asp Leu Ile
187          65          70          75
189 atc aaa ctc cat gct ctc ctt ggt aac cgg tgg tca ctg ata gct ggt 350

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190 Ile Lys Leu His Ala Leu Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly
191      80      85      90
193 aga tta cca gga aga aca gat aat gaa gtg aag aac tat tgg aat tcc 398
194 Arg Leu Pro Gly Arg Thr Asp Asn Glu Val Lys Asn Tyr Trp Asn Ser
195      95      100      105
197 cat ata aag aga aag cta atg aag atg ggg atc gat cct aat aac cat 446
198 His Ile Lys Arg Lys Leu Met Lys Met Gly Ile Asp Pro Asn Asn His
199 110      115      120      125
201 aag ttg aac caa tat cct cat cat gtt ggt ccc ctt aac ccc acc acc 494
202 Lys Leu Asn Gln Tyr Pro His His Val Gly Pro Leu Asn Pro Thr Thr
203      130      135      140
205 acc aac tcc atg gat gtg gca tgt aag ctt aga gtg tgt tca aca gac 542
206 Thr Asn Ser Met Asp Val Ala Cys Lys Leu Arg Val Cys Ser Thr Asp
207      145      150      155
209 aat gat gat ggg atc tca gat gct gca agt tat ctc gaa gac gca aca 590
210 Asn Asp Asp Gly Ile Ser Asp Ala Ala Ser Tyr Leu Glu Asp Ala Thr
211      160      165      170
213 ccg ccc act ggt ata tcc aac ttg gac ctt gat ctc aca att gct ttt 638
214 Pro Pro Thr Gly Ile Ser Asn Leu Asp Leu Asp Leu Thr Ile Ala Phe
215      175      180      185
217 cct tcg agt cct atc aag aat att att gaa gaa agc cag cag aaa aca 686
218 Pro Ser Ser Pro Ile Lys Asn Ile Ile Glu Glu Ser Gln Gln Lys Thr
219 190      195      200      205
221 gca tct att gta aca aat gat gaa gaa gaa caa tat aca gtc cct acc 734
222 Ala Ser Ile Val Thr Asn Asp Glu Glu Glu Gln Tyr Thr Val Pro Thr
223      210      215      220
225 ctt ctt ctt ttc aga tga gacaaaaaaaa aaagcctcac acatgtggag 782
226 Leu Leu Leu Phe Arg
227      225
229 attcgtgcaa aagacctaaa ggcttacgaa ggcaacatgc acgccattgt caaattcttt 842
231 tggatgatgg attgaaacca tatecttgtc cattagaaag gaggaagata agctaaaact 902
233 gtattattgt gtataaattt ggtagaaaga aagatttcaa cttaagaatt aggatcaaatt 962
235 aactgaatga atgaacgaat tgcagataag ttgttaggag gttttcaatc aacttatctg 1022
237 caattaattt ggtggagctg atgtaggatg atgagttcat cgtacatgaa ctgaaccttt 1082
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245 <211> LENGTH: 226
246 <212> TYPE: PRT
247 <213> ORGANISM: Gossypium hirsutum
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252 Ser Lys Gln Glu Asp Gln Lys Leu Ile Asp Tyr Ile Arg Ile His Gly
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254 Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu His Arg Cys
255 35 40 45
256 Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp Ile
257 50 55 60

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258 Lys Arg Gly Asn Phe Ala Gln Asp Glu Glu Asp Leu Ile Ile Lys Leu
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260 His Ala Leu Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly Arg Leu Pro
261 85 90 95
262 Gly Arg Thr Asp Asn Glu Val Lys Asn Tyr Trp Asn Ser His Ile Lys
263 100 105 110
264 Arg Lys Leu Met Lys Met Gly Ile Asp Pro Asn Asn His Lys Leu Asn
265 115 120 125
266 Gln Tyr Pro His His Val Gly Pro Leu Asn Pro Thr Thr Thr Asn Ser
267 130 135 140
268 Met Asp Val Ala Cys Lys Leu Arg Val Cys Ser Thr Asp Asn Asp Asp
269 145 150 155 160
270 Gly Ile Ser Asp Ala Ala Ser Tyr Leu Glu Asp Ala Thr Pro Pro Thr
271 165 170 175
272 Gly Ile Ser Asn Leu Asp Leu Asp Leu Thr Ile Ala Phe Pro Ser Ser
273 180 185 190
274 Pro Ile Lys Asn Ile Ile Glu Glu Ser Gln Gln Lys Thr Ala Ser Ile
275 195 200 205
276 Val Thr Asn Asp Glu Glu Glu Gln Tyr Thr Val Pro Thr Leu Leu Leu
277 210 215 220
278 Phe Arg
279 225
283 <210> SEQ ID NO: 5
284 <211> LENGTH: 1081
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286 <213> ORGANISM: Gossypium hirsutum
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289 <221> NAME/KEY: CDS
290 <222> LOCATION: (86)..(994)
291 <223> OTHER INFORMATION: GhMYB7
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297 Met Gly Arg Ser Pro Cys Cys Ser Lys
298 1 5
300 gaa ggc ctt aac aga gga gct tgg act gct ctt gaa gac aaa att ctt 160
301 Glu Gly Leu Asn Arg Gly Ala Trp Thr Ala Leu Glu Asp Lys Ile Leu
302 10 15 20 25
304 aaa gat tat atc aaa gta cac ggt gaa ggt cgt tgg aga aat ctc ccc 208
305 Lys Asp Tyr Ile Lys Val His Gly Glu Gly Arg Trp Arg Asn Leu Pro
306 30 35 40
308 aaa aga gct ggt ctt aag aga tgt ggg aaa agt tgt agg ctt cgg tgg 256
309 Lys Arg Ala Gly Leu Lys Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp
310 45 50 55
312 ttg aat tat ttg aga cct gat att aaa aga ggt aac ata tca cct gac 304
313 Leu Asn Tyr Leu Arg Pro Asp Ile Lys Arg Gly Asn Ile Ser Pro Asp
314 60 65 70
316 gag gaa gag ctt atc atc aaa ctc cac aaa ctc ttg gga aac aga tgg 352
317 Glu Glu Glu Leu Ile Ile Lys Leu His Lys Leu Leu Gly Asn Arg Trp

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Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

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Input Set : A:\Uco-956.app

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 L:447 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
 L:575 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
 L:593 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
 L:798 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
 L:827 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26